

SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

<140> 09/256,000

<141> 1999-02-23

<150> 60/075,508

<151> 1998-02-23

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 1548

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(1423)

<400> 1

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Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
10                               15                               20                               25

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
30                               35                               40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
45                               50                               55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
60                               65                               70

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
75                               80                               85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
90                               95                               100                               105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388

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Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp		
			125					130					135				
ctt	tgg	gag	ccc	aat	gag	atg	ctg	agc	tgc	ctg	gag	cac	atg	tac	cac	484	
Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His		
			140				145					150					
gac	ctc	ggg	ctg	gtc	agg	gac	ttc	agc	atc	aac	cct	gtc	acc	ctc	agg	532	
Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg		
			155			160					165						
agg	tgg	ctg	ttc	tgc	gtc	cac	gac	aac	tac	aga	aac	aac	ccc	ttc	cac	580	
Arg	Trp	Leu	Phe	Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His		
					175					180					185		
aac	ttc	cgg	cac	tgc	ttc	tgc	gtg	gcc	cag	atg	atg	tac	agc	atg	gtc	628	
Asn	Phe	Arg	His	Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val		
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tgg	ctc	tgc	agt	ctc	cag	gag	aag	ttc	tca	caa	acg	gat	atc	ctg	atc	676	
Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
			205					210					215				
cta	atg	aca	gcg	gcc	atc	tgc	cac	gat	ctg	gac	cat	ccc	ggc	tac	aac	724	
Leu	Met	Thr	Ala	Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn		
			220				225					230					
aac	acg	tac	cag	atc	aat	gcc	cgc	aca	gag	ctg	gcg	gtc	cgc	tac	aat	772	
Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn		
			235			240					245						
gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	gcc	ttc	cag	atc	820	
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile		
					255					260					265		
ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	cca	cct	gat	ggg	868	
Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly		
				270					275						280		
ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	ttg	gcc	act	gac	916	
Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp		
			285					290					295				
atg	gca	aga	cat	gca	gaa	att	atg	gat	tct	ttc	aaa	gag	aaa	atg	gag	964	
Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu		
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aat	ttt	gac	tac	agc	aac	gag	gag	cac	atg	acc	ctg	ctg	aag	atg	att	1012	
Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile		
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ttg	ata	aaa	tgc	tgt	gat	atc	tct	aac	gag	gtc	cgt	cca	atg	gaa	gtc	1060	
Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val		

330	335	340	345	
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc				1108
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser	350	355	360	
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga				1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg	365	370	375	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc				1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val	380	385	390	
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag				1252
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu	395	400	405	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag				1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu	410	415	420	425
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac				1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp	430	435	440	
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat				1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp	445	450	455	
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg				1443
Val Lys Asn Ser Glu Gly Asp Cys Ala	460	465		
gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc				1503
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<210> 2
 <211> 466
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
 35 40 45
 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
 50 55 60

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
 65 70 75 80
 Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
 85 90 95
 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
 100 105 110
 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
 115 120 125
 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
 130 135 140
 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
 145 150 155 160
 Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
 165 170 175
 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
 180 185 190
 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
 195 200 205
 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
 210 215 220
 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
 225 230 235 240
 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
 245 250 255
 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
 260 265 270
 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
 275 280 285
 Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
 290 295 300
 Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
 305 310 315 320
 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
 325 330 335
 Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
 340 345 350
 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
 355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
 370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
 385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
 405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
 420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
 435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
 450 455 460

Cys Ala
 465

<210> 3
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Nucleotides at positions 130, 186, and 205 are
 either A, T, G, or C.

<400> 3
 agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60
 accaaggcca cagcccagat tgggttcac aagtttgccc tgatcccaat gtttgaaaca 120
 gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180
 gatcgntacg aggagctgaa gcggnatagat gacgccatga aagag 225

<210> 4
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Nucleotides at positions 12, 36, 61, and 109 are
 either A, T, G, or C.

<400> 4
 gtaccagatc antgcccga cagagctggc ggtccgntac aatgacatct caccgttgga 60
 gnaaccacca ctgcgccgtg gccttcacga tctcgcgga gcctgagtgn aacatcttct 120
 ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 14, 22, and 50 are either
A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gncttccaga tctctgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411
are either A, T, G, or C.

<400> 6
nggttaactg ggcacatcttg tctttctctg agaacagcga tctggttatg gggcatttct 60
gtctctaattg tcaactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccgtggc cccgttcatg gaccgagaca aagtgaacaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tccccatggg 240
ttgagggaga ttcatgctgg cagccanttt gggaatccc gaggattcgc tacgagggag 300
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagttttga agttttgggg gggccaccga ggaagtccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,
and 396 are either A, T, G, or C.

<400> 7
nagaaaaaag tgaacaaaat ggttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60
ggagctcttc cctgcacaag gntcccgccg antcggccag cccgtccaga actgcagcca 120
cgccccccgn tttcctcagg cacagtctcc ttcaactgtt ttacatctc tgcttctctc 180
tctggacttc tcggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat ctctcctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360
gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420
aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203,
206, 238, 252, 297, 370, 389, and 427 are either
A, T, G, or C.

<400> 8
tttttttttt ttttttttgt atcagtgaac aaaatgggtc ttagaaaaca tggctcttg 60
gtncaggtg cccagggagc tcttcctgc acaaggancc cgcgcantcg gccagcccgt 120
ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180
atctctgntt ctctctctgg gantnttcgg tgggccccag aacgtcaagc tgtcagtntt 240
cttctgtaac tntttcatgg gcgtcatcta tccgtttcag ctctcctgta ggcgatnttg 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360
gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaaccaatt 420
tgggggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggagggtg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tcctgatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA

<213> Mus musculus

<400> 10

gagaatTTTtg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgtc 240
tgtccaatgt 250

<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 155, 393, and 442 are
either A, T, G, or C.

<400> 11

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aatggagaat tttgactaca gcaacgagga gcacatgacc ctggtgagtg gcttattctg 120
cctgggtggg cagccaggcg gttgggctgg cgaanaggTT catccatcca gctcacactg 180
gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggTTTT 240
caaggTcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggTcctcct 300
TcatggTcag aggcagcatt ctccatttcc tccatctcTT ttgggattTT gaaggagata 360
aagtggggTg aaggccgtgc attctcgctc tgnTTTTcca gagaattaaa accagttttc 420
ccttgaaggc acagccccag cntggcattt tgaaagtTg 459

<210> 12

<211> 599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99)..(443)

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Cys His Cys Leu Leu His
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
 Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
 10 15 20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
 25 30 35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 260
 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
 40 45 50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 308
 Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
 55 60 65 70

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 356
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
 75 80 85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 404
 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
 90 95 100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 105 110 115

ggggggcgctg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 513

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 573

ctgatacaaaa aaaaaaaaaa aaaaaa 599

<210> 13

<211> 115

<212> PRT

<213> Homo sapiens

<400> 13

Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
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Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
 35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala

85

90

95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
 100 105 110

Asp Cys Ala
 115

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

agtcgaattc accgtgagaa gtcagaag

28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gtcaaagctt acatggtctt gtggtgcc

28

<210> 16

<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)..(1066)

<400> 16

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cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115
 Ala Leu Glu
 1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
 His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
 5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50
 tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
 Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
 55 60 65
 gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
 Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
 70 75 80
 ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg 403
 Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
 85 90 95
 gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg 451
 Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
 100 105 110 115
 gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc 499
 Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
 120 125 130
 cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc 547
 Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile
 135 140 145
 ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa 595
 Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys
 150 155 160
 gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg 643
 Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu
 165 170 175
 ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt 691
 Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg
 180 185 190 195
 cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat 739
 Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr
 200 205 210
 ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg 787
 Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
 215 220 225
 ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 835
 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
 230 235 240
 atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 883
 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
 245 250 255
 ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 931

Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
 260 265 270 275

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 979
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
 280 285 290

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 1027
 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
 295 300 305

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 1076
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 310 315 320

ggggggcgctg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 1136

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 1196

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Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
 35 40 45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
 50 55 60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65 70 75 80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
 85 90 95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
 100 105 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
 130 135 140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160
 Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175
 Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190
 Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205
 Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220
 Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 225 230 235 240
 Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
 245 250 255
 Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
 260 265 270
 Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
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 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala
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 atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
 Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
 15 20 25
 tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
 Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
 30 35 40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg	253
Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met	
45 50 55 60	
gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac	301
Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr	
65 70 75	
aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta	349
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu	
80 85 90	
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc	397
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
95 100 105	
aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
110 115 120	
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	
125 130 135 140	
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc	541
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	
145 150 155	
agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag	589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
160 165 170	
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc	637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	
175 180 185	
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg	685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	
190 195 200	
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac	733
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	
205 210 215 220	
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg	781
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	
225 230 235	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac	829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	
240 245 250	
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc	877
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	
255 260 265	
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc	925

Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
270						275					280						
cta	atg	aca	gcg	gcc	atc	tgc	cac	gat	ctg	gac	cat	ccc	ggc	tac	aac	973	
Leu	Met	Thr	Ala	Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn		
285					290				295						300		
aac	acg	tac	cag	atc	aat	gcc	cgc	aca	gag	ctg	gcg	gtc	cgc	tac	aat	1021	
Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn		
				305					310					315			
gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	gcc	ctc	cag	atc	1069	
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile		
			320					325					330				
ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	cca	cct	gat	ggg	1117	
Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly		
		335				340						345					
ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	ttg	gcc	act	gac	1165	
Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp		
	350					355					360						
atg	gca	aga	cat	gca	gaa	att	atg	gat	tct	ttc	aaa	gag	aaa	atg	gag	1213	
Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu		
365					370				375						380		
aat	ttt	gac	tac	agc	aac	gag	gag	cac	atg	acc	ctg	ctg	aag	atg	att	1261	
Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile		
				385					390					395			
ttg	ata	aaa	tgc	tgt	gat	atc	tct	aac	gag	gtc	cgt	cca	atg	gaa	gtc	1309	
Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val		
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gca	gag	cct	tgg	gtg	gac	tgt	tta	tta	gag	gaa	tat	ttt	atg	cag	agc	1357	
Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser		
		415				420						425					
gac	cgt	gag	aag	tca	gaa	ggc	ctt	cct	gtg	gca	ccg	ttc	atg	gac	cga	1405	
Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg		
	430					435					440						
gac	aaa	gtg	acc	aag	gcc	aca	gcc	cag	att	ggg	ttc	atc	aag	ttt	gtc	1453	
Asp	Lys	Val	Thr	Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val		
	445				450					455					460		
ctg	atc	cca	atg	ttt	gaa	aca	gtg	acc	aag	ctc	ttc	ccc	atg	gtt	gag	1501	
Leu	Ile	Pro	Met	Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu		
				465					470					475			
gag	atc	atg	ctg	cag	cca	ctt	tgg	gaa	tcc	cga	gat	cgc	tac	gag	gag	1549	
Glu	Ile	Met	Leu	Gln	Pro	Leu	Trp	Glu	Ser	Arg	Asp	Arg	Tyr	Glu	Glu		
			480					485					490				
ctg	aag	cgg	ata	gat	gac	gcc	atg	aaa	gag	tta	cag	aag	aag	act	gac	1597	
Leu	Lys	Arg	Ile	Asp	Asp	Ala	Met	Lys	Glu	Leu	Gln	Lys	Lys	Thr	Asp		

495

500

505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 1645
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
 510 515 520

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1692
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 525 530

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1752

ctggggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca ctgataaaaa 1812

aaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt cttttaaata 1872

atatattctt atacg 1887

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<213> Homo sapiens

<400> 19

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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
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Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	180	185	190
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	195	200	205
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	210	215	220
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	225	230	235
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	245	250	255
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	260	265	270
Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	275	280	285
Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	290	295	300
Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	305	310	315
Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	325	330	335
Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	340	345	350
Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	355	360	365
Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	370	375	380
Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	385	390	395
Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	405	410	415
Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	420	425	430
Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	435	440	445
Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	450	455	460
Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu	Glu	Ile	Met	Leu	465	470	475

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
485 490 495

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Glu Gly Asp Cys Ala
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<210> 20

<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1741)

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tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu

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aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu 165 170 175			529
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aag aag atg agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195 200 205			625
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220			673
gcg gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240			721
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255			769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270			817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285			865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300			913
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cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335			1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340 345 350			1057
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365			1105

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag 1153
 Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380

tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga 1201
 Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400

cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca 1249
 Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415

gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc 1297
 Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430

aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt 1345
 Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445

gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg 1393
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460

gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca 1441
 Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480

gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag 1489
 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495

gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt 1537
 Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510

gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag 1585
 Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525

cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat 1633
 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540

gag gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg 1681
 Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
 545 550 555 560

gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa 1729
 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
 565 570 575

gga gac tgt gcc tgaggaaagc ggggggcgtg gctgcagttc tggacgggct 1781
 Gly Asp Cys Ala
 580

ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841

gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaaa ggaattcatg 1901
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 aaaaaa 1967

<210> 21
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 <212> PRT
 <213> Homo sapiens

<400> 21

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Cys	Asn	Ser	Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	20	25	30	
Pro	Arg	Asn	Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val	35	40	45	
Ser	Ile	Asp	Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys	50	55	60	
Val	Arg	Pro	Val	Ala	Ile	Lys	Gln	Leu	Ser	Ala	Asp	Val	Glu	Asp	Lys	65	70	75	80
Arg	Thr	Thr	Ser	Arg	Gly	Gln	Ser	Ala	Glu	Arg	Pro	Leu	Arg	Asp	Arg	85	90	95	
Arg	Val	Val	Gly	Leu	Glu	Gln	Pro	Arg	Glu	Gly	Ala	Phe	Glu	Ser	100	105	110		
Gly	Gln	Val	Glu	Pro	Arg	Pro	Arg	Glu	Pro	Gln	Gly	Cys	Tyr	Gln	Glu	115	120	125	
Gly	Gln	Arg	Ile	Pro	Pro	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val	Leu	130	135	140	
Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu	Leu	145	150	155	160
Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	165	170	175	
Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	180	185	190	
Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	195	200	205	
Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	210	215	220	
Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	225	230	235	240

Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	
				245					250					255		
Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	
			260					265					270			
Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	
		275					280					285				
Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	
	290					295					300					
Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	
305					310					315					320	
Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	
				325					330					335		
Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	
			340					345					350			
Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	
		355					360					365				
Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	
	370					375					380					
Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	
385					390					395					400	
Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	
				405					410					415		
Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	
			420					425					430			
Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	
		435					440					445				
Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	
	450					455					460					
Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	
465					470					475					480	
Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	
				485					490					495		
Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	
			500					505					510			
Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu	Glu	Ile	Met	Leu	Gln	
	515						520					525				
Pro	Leu	Trp	Glu	Ser	Arg	Asp	Arg	Tyr	Glu	Glu	Leu	Lys	Arg	Ile	Asp	
	530					535					540					

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
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Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
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Gly Asp Cys Ala
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ggaaagtaca gtaaaaagtc cgagtgccgc cgccggggcg agg atg gga tcc ggc 175
Met Gly Ser Gly
1

tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
5 10 15 20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
25 30 35

gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
40 45 50

ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
55 60 65

gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
70 75 80

caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
85 90 95 100

gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
105 110 115

gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga 559

Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly		
			120					125					130				
cta	aaa	gtg	gtg	gag	att	gag	aaa	tgc	aag	agt	gac	att	aag	aag	atg	607	
Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met		
		135					140					145					
agg	gag	gag	ctg	gcg	gcc	aga	agc	agc	agg	acc	aac	tgc	ccc	tgt	aag	655	
Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys		
		150					155				160						
tac	agt	ttt	ttg	gat	aac	cac	aag	aag	ttg	act	cct	cga	cgc	gat	gtt	703	
Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val		
					170					175					180		
ccc	act	tac	ccc	aag	tac	ctg	ctc	tct	cca	gag	acc	atc	gag	gcc	ctg	751	
Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu		
				185					190					195			
cgg	aag	ccg	acc	ttt	gac	gtc	tgg	ctt	tgg	gag	ccc	aat	gag	atg	ctg	799	
Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu		
			200					205					210				
agc	tgc	ctg	gag	cac	atg	tac	cac	gac	ctc	ggg	ctg	gtc	agg	gac	ttc	847	
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe		
		215					220					225					
agc	atc	aac	cct	gtc	acc	ctc	agg	agg	tgg	ctg	ttc	tgc	gtc	cac	gac	895	
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp		
		230				235					240						
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	cgg	cac	tgc	ttc	tgc	gtg	943	
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val		
		245			250				255						260		
gcc	cag	atg	atg	tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	991	
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys		
				265				270						275			
ttc	tca	caa	acg	gat	atc	ctg	atc	cta	atg	aca	gcg	gcc	atc	tgc	cac	1039	
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His		
			280					285					290				
gat	ctg	gac	cat	ccc	ggc	tac	aac	aac	acg	tac	cag	atc	aat	gcc	cgc	1087	
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg		
		295					300					305					
aca	gag	ctg	gcg	gtc	cgc	tac	aat	gac	atc	tca	ccg	ctg	gag	aac	cac	1135	
Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His		
		310				315					320						
cac	tgc	gcc	gtg	gcc	ttc	cag	atc	ctc	gcc	gag	cct	gag	tgc	aac	atc	1183	
His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile		
		325			330				335					340			
ttc	tcc	aac	atc	cca	cct	gat	ggg	ttc	aag	cag	atc	cga	cag	gga	atg	1231	
Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met		

345	350	355	
atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg			1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met			
360	365	370	
gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag			1327
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu			
375	380	385	
cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct			1375
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser			
390	395	400	
aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta			1423
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu			
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tta gag gaa tat ttt atg cag agc gac cgt gaga			1457
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg			
425	430		

<210> 23
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 <213> Homo sapiens

<400> 23

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp			
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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser			
20	25	30	
Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn			
35	40	45	
Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp			
50	55	60	
Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro			
65	70	75	80
Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val			
85	90	95	
Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu			
100	105	110	
Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val			
115	120	125	
Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp			
130	135	140	
Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn			

145		150		155		160
Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro	165		170		175	
Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr	180		185		190	
Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro	195		200		205	
Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu	210		215		220	
Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe	225		230		235	240
Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His	245		250		255	
Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser	260		265		270	
Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala	275		280		285	
Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln	290		295		300	
Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro	305		310		315	320
Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro	325		330		335	
Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile	340		345		350	
Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His	355		360		365	
Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr	370		375		380	
Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys	385		390		395	400
Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp	405		410		415	
Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg	420		425		430	

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<223> Description of Artificial Sequence: FLAG epitope

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Asp Thr Lys Asp Asp Asp Asp Lys
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<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 25

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<210> 26

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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